

**IN THE CLAIMS:**

Please amend claims 1, 3-19 and 21, as follows:

1. (Currently Amended) A method of screening a protein for involvement in cancer, comprising:
  - i) exposing the protein to a first viral oncoprotein;
  - ii) assaying for interaction of the protein and the first viral oncoprotein;
  - iii) exposing the protein to a second viral oncoprotein; and
  - iv) assaying for interaction of the protein and the second viral oncoprotein,wherein interaction of the protein with the viral oncoproteins indicates that the protein is involved in cancer.
2. (Original) The method according to claim 1, wherein only those proteins that interact with the first viral oncoprotein are exposed to the second viral oncoprotein.
3. (Currently Amended) The A method according to claim 1, wherein the protein is contained within a mixture of proteins which may or may not be involved in the aetiology of cancer.
4. (Currently Amended) The method according to ~~any preceding~~ claim 1, wherein the protein is derived from a tissue having a highly complex pattern of gene expression combined with a high capacity for proliferation.
5. (Currently Amended) The method of claim 4 wherein the tissue is selected from the group consisting of placenta, cord blood CD34<sup>+</sup> haemopoietic stem cells, and ~~or~~ foetal brain.
6. (Currently Amended) The A method according to ~~any preceding~~ claim 1, wherein those proteins that exhibit interaction with a viral oncoprotein are correlated with interactions with other oncoproteins.

7. (Currently Amended) The A method according to ~~any preceding~~ claim 1, wherein the first and second viral oncoproteins are independently selected from the group consisting of comprising human papilloma virus type 6, 16 and 18, E6, E7 and E5 proteins, hepatitis B “X”, hepatitis C “Core”, SV40 large “T” and small “T”, adenovirus “E1A” and “E1B”, human T lymphotropic virus types 1 and 2 “Tax”, Epstein Barr virus “LMP1” and “EBNA3”, and JC virus large “T” and small “T”.
8. (Currently Amended) The A method according to claim 7, wherein the first oncoprotein is HPV 16 E6.
9. (Currently Amended) The A method according to claim 7 ~~or claim 8~~, wherein the second oncoprotein is “Tax”.
10. (Currently Amended) The A method according to ~~any preceding~~ claim 1, wherein the protein is derived from a cDNA library.
11. (Currently Amended) The A method according to claim 10, wherein the primary sequence of the protein can be derived by cross reference to the nucleic acid base sequence of the parent cDNA.
12. (Currently Amended) The A method according to ~~any preceding~~ claim 1, additionally comprising a validation phase.
13. (Currently Amended) The A method according to claim 12, wherein the validation phase comprises at least one of the following further steps:
  - a) analysing expression levels of a protein, indicated as being involved in cancer, in cancerous and non-cancerous tissue samples;
  - b) comparing the levels of expression of the protein in the cancerous and non-cancerous tissues;
  - c) analysing the effects of targeted antisense or siRNA oligonucleotide mediated gene

silencing on the growth characteristics of transformed and non-transformed cell lines;

- d) analysing the effects of constitutive or inducible expression of proteins in transformed and non-transformed cell lines;
- e) analysing the effects of antibodies or intrabodies directed at one or more domains of the protein; and
- f) comparing the primary amino acid sequence of the protein or parent nucleic acid base sequence with one or more databases of known sequences of other proteins to identify homology with functional domains and infer putative involvement in cancer.

- 14. (Currently Amended) The A method according to claim 12, wherein the validation step comprises analysis of nucleic acids derived from a tissue sample, tumour biopsy or cell line for the presence of mutant forms of the nucleic acids encoding a protein indicated as being involved in cancer.
- 15. (Currently Amended) The A method according to claim 12, wherein the validation phase comprises analysis of DNA derived from a tissue sample, tumour biopsy, or cell line for the presence of mutant forms of the DNA encoding a protein indicated as being involved in cancer.
- 16. (Currently Amended) The A method according to ~~any preceding~~ claim 1, further comprising:
  - v) exposing a protein identified as a protein involved in cancer ~~according to claim 1~~ to a protein sample; and
  - vi) assaying for interaction of proteins within the sample with the protein identified as involved in cancer ~~according to claim 1~~;wherein proteins identified in step vi) are secondary protein targets involved with cancer.
- 17. (Currently Amended) The A method according to claim 16, wherein the second protein is derived from the same tissue as the protein exposed to the viral oncoproteins.

18. (Currently Amended) ~~The~~ A method according to ~~any preceding~~ claim 1, wherein the protein indicated to be involved with cancer is selected as a target for modulation for therapy for cancer.
19. (Currently Amended) ~~The~~ A method according to ~~any preceding~~ claim 1, wherein the protein indicated to be involved with cancer is selected as a marker for the diagnosis of cancer.
20. (Original) A method of screening a protein sample to identify proteins that are secondary protein targets for viral oncoproteins comprising:
- i) exposing protein identified as a protein involved in cancer according to claim 1 to the protein sample; and
  - ii) assaying for interaction of proteins within the sample with proteins identified by their interaction with viral oncoproteins according to claim 1;
- wherein proteins identified by their interaction with the protein involved in cancer in step ii) represent secondary protein targets involved with cancer.
21. (Currently Amended) The method of claim 20, further comprising the step of:
- iii) ~~investigating~~ Investigating the functional validation of the secondary targets in cancer by at least one of the following further steps: ~~the according to the steps defined by claim 13~~
    - a) analysing expression levels of a protein, indicated as being involved in cancer, in cancerous and non-cancerous tissue samples;
    - b) comparing the levels of expression of the protein in the cancerous and non-cancerous tissues;
    - c) analysing the effects of targeted antisense or siRNA oligonucleotide mediated gene silencing on the growth characteristics of transformed and non-transformed cell lines;
    - d) analysing the effects of constitutive or inducible expression of proteins in transformed and non-transformed cell lines;
    - e) analysing the effects of antibodies or intrabodies directed at one or more domains of the protein; and
    - f) comparing the primary amino acid sequence of the protein or parent nucleic acid base

sequence with one or more databases of known sequences of other proteins to identify homology with functional domains and infer putative involvement in cancer.